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Identification of high yielding genotypes in greengram (*Vigna radiata* L.)

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Abstract

Greengram is a vital pulse crop throughout Asia, Australia, West Indies, South and North America, tropical and subtropical Africa. Owing to its high protein content greengram is an important part of diet. Low productivity is the major constraint in increasing area under greengram crop. Genetic variability is the pre-requisite for developing high yielding cultivar. Assessment of genetic variability is a preliminary step. With this background investigation was conducted to identify high yielding genotype. 81 genotypes were screened for yield and its attributing traits and assessed for genetic variability. Analysis of variance revealed significant mean squares attributable to genotypes for all the characters studied except primary branches plant^{-1}, number of clusters plant^{-1} and 100 seed weight. Based on performance 13 genotypes were selected as high yielding.

Keywords: greengram, genotypes, variability

Introduction

Greengram [*Vigna radiata* (L.) Wilczek], commonly known as greengram or mungbean is a vital crop grown throughout Asia, Australia, West Indies, South and North America, tropical and subtropical Africa. Greengram is native to Indo-Burma region of South-East Asia (Vavilov, 1951). Greengram is one of the thirteen food legumes grown in India and third most important pulse crop of India after chickpea and pigeonpea. Greengram is a short duration legume crop cultivated primarily for its dry seeds. India is the major producer of greengram in the world and grown in almost all the states. It is grown in 4.24 m ha with the production of 20.23 m t and 477 Kg ha^{-1} productivity.

Greengram is the important source of dietary protein. Greengram contains carbohydrates (51%), protein (24%), minerals (4%) and vitamins (3%). Owing to low cost, greengram is easily affordable and accessible by all classes of society. Besides, it has the remarkable quality of serving the symbiotic root rhizobia to fix atmospheric nitrogen and augments soil fertility. Declaration of 2016 as 'International year of pulses' by Food and Agriculture Organization substantiates increasing emphasis on pulse crops. Inspite of importance communicated enormously, standard worldwide yield of mungbean is very low (477 kg ha^{-1}) and its production has not considerably increased yet. Lack of variability in greengram is one of the major impediments in greengram crop improvement. Assessment of variability is pre-requisite to identify high yielding genotypes. With this background present investigation was conducted to identify high yielding genotypes.

Material and method

Set of 81 genotypes were planted in augmented design during *Kharif*-2018 at the experimental plots of Department of Genetics and Plant Breeding (GPB), College of Agriculture, Shivamogga. Genotypes and three checks (KKM-3, YADADRI and BGS-9) were raised in nine blocks in a row length of 1.5 m with 30 cm spacing between rows and 10 cm spacing between plants in a row. Data were recorded on five randomly selected plants of each inbred line for the following traits based on counting/measurement using appropriate scale depending on the traits.

Results and Discussion

Variability for yield and its component traits among the genotypes under study was assessed through analysis of variance (ANOVA) and estimates of variability parameters. Analysis of variance (ANOVA) revealed significant mean squares attributable to genotypes for all the characters studied except primary branches plant^{-1}, number of clusters plant^{-1} and 100 seed weight (Table 1). Mean squares due to 'genotypes vs. checks' were significant for all the traits except number of pods cluster^{-1} and 100 seed weight. These results are in agreement with those of Kumar *et al.* (2010) [5]; Ahmad *et al.* (2014) [1]; Singh *et al.* (2014); Titumeer *et al.* (2014) and Garg *et al.* (2017) [2]. ANOVA is the preliminary step that indicates presence of variability among the genotypes under investigation. Significant differences among the genotypes justifies quantification of variability.

Days to 50 per cent flowering

Estimates of GCV (8.98%) and PCV (9.16%) were lower; while that of broad-sense heritability (96.04%) was found high and expected GAM (18.13%) was moderate.

Plant height

Lower estimates of GCV (6.32%), broad-sense heritability (6.70%) and expected GAM (3.37%) coupled with higher estimate of PCV (24.44%) were recorded.

Primary branches plant^{-1}

Lower estimates of GCV (3.58%), PCV (7.18%), broad-sense heritability (24.90%) and expected GAM (3.68%) were recorded.

Secondary branches plant^{-1}

Moderate estimates of GCV (16.34%), PCV (17.02%) and higher estimates of broad-sense heritability (92.10%) and expected GAM (32.29%) were recorded.

Number of clusters plant^{-1}

Higher estimates of GCV (46.04%), PCV (47.32%), broad-sense heritability (94.68%) and expected GAM (92.29%) were recorded.

Number of pods cluster^{-1}

Moderate estimates of GCV (16.51%) and broad-sense heritability (36.08%) coupled with higher estimates of PCV (27.49%) and expected GAM (20.43%) were recorded.

Number of pods plant^{-1}

Higher estimates of GCV (38.65%), PCV (39.58%), broad-sense heritability (95.32%) and expected GAM (77.73%) were recorded.

Pod length

Higher estimates of GCV (28.72%), PCV (30.52%), broad-sense heritability (88.53%) and expected GAM (55.66%) were recorded.

Number of seeds pod^{-1}

Moderate estimates of GCV (10.82%), PCV (12.13%) and expected GAM (19.89%) were recorded. Further, higher estimate of broad-sense heritability (79.60%) was recorded.

Seed yield plant^{-1}

Higher estimates of GCV (46.12%), PCV (48.66%), broad-sense heritability (89.85%) and expected GAM (90.079%) were recorded.

100 seed weight

Lower estimates of GCV (6.57%), broad sense heritability (15.07%) and expected GAM (5.25%) coupled with moderate estimate of PCV (16.93%) were recorded.

If most of the variability is attributable to non-heritable portion of variability, selection of genotypes will not lead to improvement. Higher estimates of PCV indicate larger contribution of environment in manifesting the phenotype. While lower estimates of PCV indicate minimal influence of environment on manifestation of that particular trait. Therefore, efficiency of selection depends on the degree of correspondence between the estimates of phenotypic coefficient of variation and the genotypic coefficient of variation.

In the present study traits *viz.*, number of clusters plant^{-1}, number of pods plant^{-1}, pod length, seed yield plant^{-1} revealing higher estimates of both PCV and GCV, traits showing moderate estimates of PCV and GCV (Secondary branches plant^{-1} and number of seeds pod^{-1}) and Days to 50 *per cent* flowering showing lower estimates of both PCV and GCV are ought to exhibit close correspondence between PCV and GCV (Table 2). Close correspondence between PCV and GCV indicates insignificant influence of environment on the trait. These results are in agreement with those of Kumar *et al*. (2010) [6]; Singh *et al*. (2014) [5]; Garg *et al*. (2017) [3]; Jagdhane *et al*. (2017) [4]; Rasal and Parhe (2017) and Azam *et al*. (2018) [2].

The concept of broad-sense heritability is useful if interest is in relative importance of genotype and environment in the determination of phenotypic values. Broad-sense heritability is the ratio of variance due to hereditary differences (σ^2_g) to the total phenotypic variance (σ^2_p) expressed in *per cent* (Lush, 1943) [7]. If the estimate of broad-sense heritability is high, trait is considered to be highly heritable. On the other hand, if it is lower, environment is considered as major factor in manifesting the trait. Traits with higher estimate of broad-sense heritability *viz*., Days to 50 *per cent* flowering, Secondary branches plant^{-1}, number of clusters plant^{-1}, number of pods plant^{-1}, pod length, number of seeds pod^{-1}, seed yield plant^{-1} have got classified into same category (low, medium or high) for both PCV and GCV (Table 2).

Estimates of broad-sense heritability along with that of expected GAM is more reliable for predicting the efficiency of selection. Higher estimates of heritability coupled with higher estimates of expected GAM indicate effectiveness of phenotype-based selection. Higher estimates of broad-sense heritability and expected GAM were recorded for secondary branches plant^{-1}, number of clusters plant^{-1}, number of pods plant^{-1}, pod length and seed yield plant^{-1}. These results are supported by similar studies carried out by Singh *et al*. (2014) [9]; Kumar and Katiyar (2015) [6]; Garg *et al*. (2017) [3]; Rasal and Parhe (2017). Based on the mean performance, 13 genotypes were selected as productive lines (Table 3).

Table 1: ANOVA for grain yield and its component traits for 81 greengram [*Vigna radiata* (L.) Wilczek] genotypes evaluated at Shivamogga during *Kharif*-2018

Source of Variation	**Degrees of freedom**	**Mean Sum of Square**										
		DFF	**PH**	**PBP**	**SBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**SYP**	**100SW**
Block (Ignoring treatments)	08	54.57**	203.92**	0.04	0.61**	36.39**	3.26*	172.78**	5.87***	3.56**	32.40**	1.52**
Genotypes + Checks (Ignoring blocks)	83	45.05**	86.37**	0.03	0.64**	19.81**	1.67	494.32**	9.06**	3.26**	119.82**	0.34
Genotypes	80	18.36**	77.30**	0.03	0.66**	18.45**	1.67	143.89**	8.46**	2.06**	44.79**	0.34
Checks	2	66.92**	42.33**	0.03	0.01	12.92**	2.11	417.44**	1.07	39.55**	22.37**	0.44
Checks *vs.* Genotypes	1	2136.49**	900.00**	0.60**	0.22*	142.14**	0.44	28682.05**	72.68**	26.89**	6317.07**	0.01
Error	16	0.59	0.54	0.02	0.69	0.80	0.98	5.48	0.80	0.35	3.74	0.28

* - Significant @ 5%; ** - Significant @ 1%

DFF	=	**Days to 50% flowering**	**NCP**	=	**Number of clusters plant^{-1}**	**NSP**	=	**Number of seeds pod^{-1}**
PH	=	Plant height (cm)	NPC	=	Number of pods cluster^{-1}	SYP	=	Seed yield plant^{-1}
PBP	=	Primary branches plant^{-1}	NPP	=	Number of pods plant^{-1}			
SBP	=	Secondary branches plant^{-1}	PL	=	Pod length			

Table 2: Estimates of parameters specifying variability for grain yield and its component traits for 81 greengram [*Vigna radiata* (L). Wilczek] genotypes evaluated at Shivamogga during *Kharif*-2018

Sl. No.	Traits	Mean	Range		SR	GCV (%)	PCV (%)	h^2(bs) (%)	GAM
			Lowest	Highest					
1	Days to 50% flowering	39.63	28.00	51.40	0.59	8.98	9.16	96.04	18.13
2	Plant height	31.44	18.10	57.80	1.26	6.32	24.44	6.70	3.37
3	Primary branches plant^{-1}	2.28	1.80	2.60	0.35	3.58	7.18	24.90	3.68
4	Secondary branches plant^{-1}	4.28	0.50	7.40	1.61	16.34	17.02	92.10	32.29
5	Number of clusters plant^{-1}	8.86	2.40	20.60	2.05	46.04	47.32	94.68	92.29
6	Number of pods cluster^{-1}	4.56	2.20	8.40	1.36	16.51	27.49	36.08	20.43
7	Number of pods plant^{-1}	27.36	8.15	54.87	1.71	38.65	39.58	95.32	77.73
8	Pod length	8.21	1.20	15.70	1.77	28.72	30.52	88.53	55.66
9	Number of seeds pod^{-1}	11.14	6.40	14.80	0.75	10.82	12.13	79.60	19.89
10	Seed yield plant^{-1} (g)	12.49	2.31	28.42	2.09	46.12	48.66	89.85	90.07
11	100 seed weight (g)	3.37	2.80	4.40	0.77	6.57	16.93	15.07	5.25

SR	=	Standardized range
GCV	=	Genotypic coefficient of variation
PCV	=	Phenotypic coefficient of variation
h^2(bs)	=	Broad sense heritability
GAM	=	Genetic advance as *per cent* mean

Table 3: Seed yield plant^{-1} of top performing greengram [*Vigna radiata* (L). Wilczek] genotypes

Sl No.	Genotype	Seed yield plant^{-1} (g)
1	KM-17-211	25.76
2	KM-17-191	24.32
3	KM-17-183	23.17
4	GG-16-4	22.31
5	RM-16-16	23.17
6	JNG-18	24.39
7	PM-110	24.28
8	RM-16-15	22.28
9	LGG-410	26.13
10	GG-16-10	20.98
11	TK-6-1	25.37
12	Yadadri (check)	31.27
13	IPM 205-7	28.42

Conclusion

Variability is pre-requisite for selection. Assessment of variability is the preliminary step in identifying productive genotype. In the present investigation variability was assessed for a set of 81 genotypes and 13 genotypes were identified as high yielding based on seed yield plant^{-1}.

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